13

Page: 1

## Raw Sequence Listing

04/08/93 07:45:45 S5136.raw

		' ' ' '
1		SEQUENCE LISTING
2		
3	(1) GENERAL I	INFORMATION:
4	(,	
5 6	(i) APPI	ICANT: Burkly, Linda C.
7	(ii) TITI	E OF INVENTION: Treatment for Insulin Dependent Diabetes
9 10	(iii) NUME	BER OF SEQUENCES: 8
11	(iv) COPE	RESPONDENCE ADDRESS:
12	• • • • • • •	ADDRESSEE: Allegretti & Witcoff, Ltd.
13		STREET: 10 South Wacker Drive, Suite 3000
14		CITY: Chicago
15	× .	STATE: IL
16	••	COUNTRY: US
17	• •	ZIP: 60606
18	(F)	Z1P: 00000
19	/**\ COME	PUTER READABLE FORM:
20	• •	MEDIUM TYPE: Floppy disk
21		COMPUTER: IBM PC compatible
22		OPERATING SYSTEM: PC-DOS/MS-DOS
23		SOFTWARE: PatentIn Release #1.0, Version #1.25
24	(D)	DOFTHAND. Fatencin Release WI.U, Version WI.23
25	(vi) CURR	ENT APPLICATION DATA:
26	•	APPLICATION NUMBER:
27		FILING DATE: 9 February 1993
28		CLASSIFICATION:
29	<b>,</b> -,	
30	(viii) ATTO	RNEY/AGENT INFORMATION:
31	(A)	NAME: McNicholas, Janet M.
32	(B)	REGISTRATION NUMBER: 32,918
33	(C)	REFERENCE/DOCKET NUMBER: 92,749; D015 US
34		
35	(ix) TELE	COMMUNICATION INFORMATION:
36	(A)	TELEPHONE: 312-715-1000
37	(B)	TELEFAX: 312-715-1234
38		
39	(2) INFORMATI	ON FOR SEQ ID NO:1:
40	(1) =====	
41		ENCE CHARACTERISTICS:
42 43		LENGTH: 360 base pairs
44		TYPE: nucleic acid
45		STRANDEDNESS: single
46	(U)	TOPOLOGY: linear
47	(ii) MOLE	CULE TYPE: cDNA
48	(ix) FEA	
49		NAME/KEY: misc_feature ,
50		LOCATION: 1
51		OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
52	ν-,	chain variable region; amino acid 1 is Glu (E) but Gln (Q)

# Raw Sequence Listing

04/08/93 07:45:46 S5136.raw

53				r	nay l	e s	ubst	itut	ed"								
54					_												
55		(ix)		ATURI													
56				A) NZ													
57			(1	3) L(	CAT	ION:	1	360									
58																	
59		(xi)	SEÇ	QUENC	CE DE	3SCR	[PTI	ON:	SEQ :	ID NO	0:1:						
60																	
61				CAG													48
62	_	Lys	Leu	Gln		Ser	GIY	Ala	GIu		Val	Lys	Pro	GIA		Ser	
63	2				6					11					16		
64																	
65				TCC													96
66	Val	Lys	Leu	Ser	Cys	Thr	Ala	ser		Phe	Asn	IIe	гув		Thr	Tyr	
67				21					26					31			
68	3 ma	<b>a.</b> a	maa	ama		~~		00m	~~~	<b>a.</b> a	~~~	cm c	a.a	maa	3 000	aas	144
69 70				GTG													144
70	Met	HIS	_	Val	гув	GIII	Arg		GIU	GIII	GIY	Leu		irp	TIE	GIA	
71 72			36					41					46				
73	N.C.C	א חיים	CATE	CCT	ccc	3 CT	aaa	CAT	7 CT	***	ጥአጥ	CAC	ccc	3 3 C	ጥጥር	CAC	192
74				Pro													192
75	ALG	51	мар	PIO	Ala	Ser	56	veħ	1111	пуь	TYL	61	FLO	пуs	riie	GIII	
76		31					30					01					
77	GTC	DAG	GCC	ACT	ΔТТ	ACA	GCG	GAC	ACG	TCC	TCC	AAC	ACA	GCC	TGG	CTG	240
78				Thr													
79	66	-2-				71					76					81	
80																	
81																	
82	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	ACT	GCC	GTC	TAC	TAC	TGT	GCA	288
83	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
84					86					91					96		
85																	
86	GAC	GGA	ATG	TGG	GTA	TCA	ACG	GGA	TAT	GCT	CTG	GAC	TTC	TGG	GGC	CAA	336
87	Asp	Gly	Met	Trp	Val	Ser	Thr	Gly	Tyr	Ala	Leu	Asp	Phe	$\mathtt{Trp}$	Gly	Gln	
88				101					106					111			
89																	
90				GTC													360
91	Gly	Thr		Val	Thr	Val	Ser										
92			116					121									
93															-		
94	(2)	INFO	RMAT	CION	FOR	SEQ	ID 1	10:2	:								
95																	
96		,	(1) 5	SEQUE													
97							: 120			acida	5						
98							amino										
99 100				(D)	TOP	·OTO(	3Y: ]	ınea	1 <i>I</i>								
101		, <u>.</u>	41 -	AOT P	ם זוזי	quypr	2. m-	oto-	i <b>n</b>								
101		( )	L T / E	IOLEC	-OTIE	1121	2: b1	.oce	r11								
102		1-	ci) q	EQUE	SNCE	חופים	יםדקי	יאסדי	. gr/	חד נ	NO · 1						
104		(2	/ K	201		2200			,	, 10	240.2	- •					

### Raw Sequence Listing

04/08/93 07:45:46 S5136.raw

105 106 107	Val 2	Lys	Leu	Gln	Gln 6	Ser	Gly	Ala	Glu	Leu 11	Val	Lys	Pro	Gly	Ala 16	Ser	
108 109 110	Val	Lys	Leu	Ser 21	Сув	Thr	Ala	Ser	Gly 26	Phe	Asn	Ile	Lys	Asp 31	Thr	Tyr	
111 112 113	Met	His	Trp 36	Val	Lys	Gln	Arg	Pro 41	Glu	Gln	Gly	Leu	Glu 46	Trp	Ile	Gly	
114 115 116	Arg	Ile 51	Asp	Pro	Ala	Ser	Gly 56	Asp	Thr	Lys	Tyr	Asp 61	Pro	Lys	Phe	Gln	
117 118 119	Val 66	Lys	Ala	Thr	Ile	Thr 71	Ala	Asp	Thr	Ser	Ser 76	Asn	Thr	Ala	Trp	Leu 81	
120 121 122	Gln	Leu	Ser	Ser	Leu 86	Thr	Ser	Glu	Asp	Thr 91	Ala	Val	Tyr	Tyr	Сув 96	Ala	
123 124 125	Asp	Gly	Met	Trp 101	Val	Ser	Thr	Gly	Tyr 106	Ala	Leu	Asp	Phe	Trp 111	Gly	Gln	
126 127 128	Gly	Thr	Thr 116	Val	Thr	Val	Ser	Ser 121									
129 130 131	(2)		ORMAT SEQ			_											
132 133			(I	3) T	INGTI	nucl	leic	acid	i	5							
134 135 136					POLC				эте								
137 138 139			MOI			PE:	CDNA	<b>\</b>									
140 141		(231)	(2	A) N2	AME/F CATI			318									
142 143 144			(1	0) 01	THER vai		RMAT Le re			oduo	ct= '	'HP1/	/2 1i	ight	chai	in	
145 146		(ix)		A) N2	AME/F			_fea	ture	•							
147 148 149						INFO					"pBA	AG172	2 ins	sert:	HP1	l/2 light	
150 151 152		(xi)	SEÇ	QUENC	CE DE	SCRI	PTIC	N: S	SEQ 1	D NC	):3:						
153 154	Ser		GTG Val		Thr					Phe					Ala		48
155 156	1				5					10					15		

### Raw Sequence Listing

04/08/93 07:45:47 S5136.raw

157				ACC													96
158	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys		Ser	Gln	Ser	Val	Thr	Asn	Asp	
159				20					25					30			
160																	
161	GTA	GCT	TGG	TAC	CAA	CAG	AAG	CCA	GGG	CAG	TCT	CCT	AAA	CTG	CTG	ATA	144
162	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	
163			35					40					45				
164																	
165	TAT	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGA	GTC	CCT	GAT	CGC	TTC	ACT	GGC	192
166	Tvr	Tvr	Ala	Ser	Asn	Arq	Tyr	Thr	Gly	Val	Pro	qaA	Arq	Phe	Thr	Gly	
167	-2-	50				J	55					60	•			•	
168																	
169	ልርጥ	GGA	тат	GGG	ACG	СУТ	ттс	ΔСТ	ጥጥር	ACC	ATC	AGC	ACT	GTG	CAG	GCT	240
170				Gly													2.0
171		GIY	TYL	GIY	1111	70	FIIC	1111	rne	1111	75	Der	1111	Val	GIII	80	
	65					70					15					80	
172																	200
173				GCA													288
174	Glu	Asp	Leu	Ala		Tyr	Phe	Сув	Gln		Asp	Tyr	Ser	Ser		Tyr	
175					85					90					95		
176																	
177	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAG	ATC							318
178	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile							
179				100					105								
180																	
181	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	10:4	:								
182																	
183			(i) :	SEOUI	NCE	CHAI	RACTI	RIST	rics	:							
183 184			(i) :	SEQUI							3						
184			(i) :	(A)	LEI	GTH:	: 106	am:	ino a		3						
184 185			(i) :	(A)	LEI TYI	NGTH:	: 106	am:	ino a id		3						
184 185 186			(i) :	(A)	LEI TYI	GTH:	: 106	am:	ino a id		3						
184 185 186 187				(A) (B) (D)	LEI TYI	NGTH: PE: 6	: 106 amino 3Y: ]	am: ac: Linea	ino a id ar		3						
184 185 186 187 188				(A)	LEI TYI	NGTH: PE: 6	: 106 amino 3Y: ]	am: ac: Linea	ino a id ar		3						
184 185 186 187 188 189		(:	ii) 1	(A) (B) (D)	LEI TYI TOI	NGTH: PE: 6 POLOC	: 106 amino GY: 3	ami aci linea	ino a id ar in	acida					•		
184 185 186 187 188 189		(:	ii) 1	(A) (B) (D)	LEI TYI TOI	NGTH: PE: 6 POLOC	: 106 amino GY: 3	ami aci linea	ino a id ar in	acida		ł:					
184 185 186 187 188 189 190		(:	ii) l ki) ¦	(A) (B) (D) MOLE(	LEI TYI TOI CULE	NGTH: PE: 6 POLOG  TYPI  DESG	: 106 amino SY: 3 S: pr	o aci linea rote:	ino a id ar in	acida	<b>NO:</b> 4		vv. 1	<b>G</b>		<b></b>	
184 185 186 187 188 189 190 191		(:	ii) l ki) ¦	(A) (B) (D)	LENCE Thr	NGTH: PE: 6 POLOG  TYPI  DESG	: 106 amino SY: 3 S: pr	o aci linea rote:	ino a id ar in	acids Q ID Phe	<b>NO:</b> 4		Val	Ser		Gly	
184 185 186 187 188 189 190 191 192	Ser 1	(:	ii) l ki) ¦	(A) (B) (D) MOLE(	LEI TYI TOI CULE	NGTH: PE: 6 POLOG  TYPI  DESG	: 106 amino SY: 3 S: pr	o aci linea rote:	ino a id ar in	acida	<b>NO:</b> 4		Val	Ser	Ala 15	Gly	
184 185 186 187 188 189 190 191 192 193	1	(: (z Ile	ii) 1 ki) 1 Val	(A) (B) (D) MOLEC	LENCE Thr	NGTH: PE: 2 POLOG  TYPI  DESG	: 106 amino SY: D S: pr CRIPT	o ami o aci linea rote: rION:	ino a id ar in : SE(	Q ID Phe	NO:4	Leu			15		
184 185 186 187 188 189 190 191 192 193 194 195	1	(: (z Ile	ii) 1 ki) 1 Val	(A) (B) (D) MOLEC SEQUI	LENCE Thr	NGTH: PE: 2 POLOG  TYPI  DESG	: 106 amino SY: D S: pr CRIPT	o ami o aci linea rote: rION:	ino a id ar in : SE( Lys	Q ID Phe	NO:4	Leu		Thr	15		
184 185 186 187 188 189 190 191 192 193 194 195 196	1	(: (z Ile	ii) 1 ki) 1 Val	(A) (B) (D) MOLEC	LENCE Thr	NGTH: PE: 2 POLOG  TYPI  DESG	: 106 amino SY: D S: pr CRIPT	o ami o aci linea rote: rION:	ino a id ar in : SE(	Q ID Phe	NO:4	Leu			15		
184 185 186 187 188 189 190 191 192 193 194 195 196	1	(: (z Ile	ii) 1 ki) 1 Val	(A) (B) (D) MOLEC SEQUI	LENCE Thr	NGTH: PE: 2 POLOG  TYPI  DESG	: 106 amino SY: D S: pr CRIPT	o ami o aci linea rote: rION:	ino a id ar in : SE( Lys	Q ID Phe	NO:4	Leu		Thr	15		
184 185 186 187 188 189 190 191 192 193 194 195 196 197	1 Asp	(: (z Ile Arg	ii)   ki)   Val	(A) (B) (D) MOLEC SEQUI	LENCE CULE Thr 5	OGTH: PE: 6 POLOG  TYPI  DESC  Gln  Thr	: 106 amino EY: ] E: pr CRIPT Thr	o actioned cote:	ino a id ar in : SE( Lys Ala 25	Q ID Phe 10 Ser	NO:4	Leu Ser	Val	Thr 30	15 Asn	Asp	
184 185 186 187 188 189 190 191 192 193 194 195 196	1 Asp	(: (z Ile Arg	ii)   ki)   Val	(A) (B) (D) MOLEC SEQUI	LENCE CULE Thr 5	OGTH: PE: 6 POLOG  TYPI  DESC  Gln  Thr	: 106 amino EY: ] E: pr CRIPT Thr	o actioned cote:	ino a id ar in : SE( Lys Ala 25	Q ID Phe 10 Ser	NO:4	Leu Ser	Val	Thr 30	15 Asn	Asp	
184 185 186 187 188 189 190 191 192 193 194 195 196 197	1 Asp	(: (z Ile Arg	ii) 1 ki) 8 Val Val	(A) (B) (D) MOLEC SEQUI	LENCE Thr 5	OGTH: PE: 6 POLOG  TYPI  DESC  Gln  Thr	: 106 amino EY: ] E: pr CRIPT Thr	o actions cotes rotes rotes rotes roy Pro	ino a id ar in : SE( Lys Ala 25	Q ID Phe 10 Ser	NO:4	Leu Ser	Val Lys	Thr 30	15 Asn	Asp	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198	1 Asp Val	(: (1 Ile Arg	ii) 1 ki) 8 Val Val Trp 35	(A) (B) (D) MOLEC SEQUI	TYIOULE ENCE Thr 5	TYPE  Gln  Gln	: 106 amino GY: 1 G: pr CRIPT Thr Cys	o actions cotes rotes rotes rotes roy Pro Lys Pro 40	ino aid ar in : SE( Lys Ala 25	Q ID Phe 10 Ser	NO:4 Leu Gln Ser	Leu Ser Pro	Val Lys 45	Thr 30 Leu	15 Asn Leu	Asp	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	1 Asp Val	(: (1 Ile Arg	ii) 1 ki) 8 Val Val Trp 35	(A) (B) (D) MOLEC SEQUI Met Thr 20	TYIOULE ENCE Thr 5	TYPE  Gln  Gln	: 106 amino GY: 1 G: pr CRIPT Thr Cys	o actions cotes rotes rotes rotes roy Pro Lys Pro 40	ino aid ar in : SE( Lys Ala 25	Q ID Phe 10 Ser	NO:4 Leu Gln Ser	Leu Ser Pro	Val Lys 45	Thr 30 Leu	15 Asn Leu	Asp	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201	1 Asp Val	(: (z Ile Arg Ala Tyr	ii) 1 ki) 8 Val Val Trp 35	(A) (B) (D) MOLEC SEQUI Met Thr 20	TYIOULE ENCE Thr 5	TYPE  Gln  Gln	: 106 amino GY: 3 GRIPT Thr Cys Lys	o actions cotes rotes rotes rotes roy Pro Lys Pro 40	ino aid ar in : SE( Lys Ala 25	Q ID Phe 10 Ser	NO:4 Leu Gln Ser	Leu Ser Pro	Val Lys 45	Thr 30 Leu	15 Asn Leu	Asp	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202	1 Asp Val Tyr	(: (z Ile Arg Ala Tyr 50	ii) 1  Val  Val  Trp  35	(A) (B) (D) MOLEC SEQUI Met Thr 20	TYION TON TON TON TON TON TON TON TON TON T	OGTH: PE: 6 POLOG  TYPH  DESC  Gln  Thr  Gln  Arg	: 106 amino EY: 3 ERIPT Thr Cys Lys Tyr 55	o actions cote: FION: Pro Lys Pro 40	ino aid ar in SE( Lys Ala 25 Gly Gly	Q ID Phe 10 Ser Gln	NO:4 Leu Gln Ser	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe	15 Asn Leu Thr	Asp Ile Gly	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203	1 Asp Val Tyr	(: (z Ile Arg Ala Tyr 50	ii) 1  Val  Val  Trp  35	(A) (B) (D) MOLEC SEQUI Met Thr 20 Tyr	TYION TON TON TON TON TON TON TON TON TON T	OGTH: PE: 6 POLOG  TYPH  DESC  Gln  Thr  Gln  Arg	: 106 amino EY: 3 ERIPT Thr Cys Lys Tyr 55	o actions cote: FION: Pro Lys Pro 40	ino aid ar in SE( Lys Ala 25 Gly Gly	Q ID Phe 10 Ser Gln	NO:4 Leu Gln Ser	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe	15 Asn Leu Thr	Asp Ile Gly	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205	1 Asp Val Tyr	(: (z Ile Arg Ala Tyr 50	ii) 1  Val  Val  Trp  35	(A) (B) (D) MOLEC SEQUI Met Thr 20 Tyr	TYION TON TON TON TON TON TON TON TON TON T	MGTH: PE: 6 POLOG  TYPE  DESC  Gln  Thr  Gln  Arg	: 106 amino EY: 3 ERIPT Thr Cys Lys Tyr 55	o actions cote: FION: Pro Lys Pro 40	ino aid ar in SE( Lys Ala 25 Gly Gly	Q ID Phe 10 Ser Gln	NO:4 Leu Gln Ser Pro	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe	15 Asn Leu Thr	Asp Ile Gly Ala	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206	1 Asp Val Tyr Ser 65	(: (1 Ile Arg Ala Tyr 50 Gly	ii)   ki)   Val Val Trp 35 Ala	(A) (B) (D) MOLEC SEQUI Met Thr 20 Tyr Ser	Thr Sle Gln Asn	TYPE DESC Gln Thr Arg Asp	: 106 amino GY: 1 G: pr CRIPT Thr Cys Lys Tyr 55 Phe	o accilines cote: FION: Pro Lys Pro 40 Thr	ino aid ar in ESEG Lys Ala 25 Gly Gly Phe	Q ID Phe 10 Ser Gln Val	NO:4 Leu Gln Ser Pro	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe Val	15 Asn Leu Thr	Asp Ile Gly Ala 80	
184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205	1 Asp Val Tyr Ser 65	(: (1 Ile Arg Ala Tyr 50 Gly	ii)   ki)   Val Val Trp 35 Ala	(A) (B) (D) MOLEC SEQUI Met Thr 20 Tyr	Thr Sle Gln Asn	TYPE DESC Gln Thr Arg Asp	: 106 amino GY: 1 G: pr CRIPT Thr Cys Lys Tyr 55 Phe	o accilines cote: FION: Pro Lys Pro 40 Thr	ino aid ar in ESEG Lys Ala 25 Gly Gly Phe	Q ID Phe 10 Ser Gln Val	NO:4 Leu Gln Ser Pro	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe Val	15 Asn Leu Thr	Asp Ile Gly Ala 80	

### Raw Sequence Listing

04/08/93 07:45:48 S5136.raw

209																	
210	Thr	Phe	Gly	_	Gly	Thr	Lys	Leu		Ile							
211				100					105								
212																	
213	(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:5	:								
214																	
215		(i)	) SE(	_													
216				A) Li						S							
217			-	B) T													
218				C) S					gle								
219			(1	D) T	OPOL	OGY:	line	ear									
220		,															
221		(11)	) MOI	LECU	LE T	YPE:	CDN	A.									
222					_												
223		(1X)	) FEZ														
224				A) N					cide								
225			(1	B) L(	JCAT.	TON:	1:	5 /					•				
226		/ \			-												
227 228		(1X)	) FEZ			7 T3 7 .											
				A) N			_		crae								
229 230			(1	B) L	JCAI.	LON:	50.	.423									
231		( + )	) FEA	ו מדזים א	₽.												
232		(14,		A) N		ZEV.	CDG										
232				B) L(				429									
234			(1	5, E	JCAI.	LOIN.	1	143									
235		(ix)	) FE	ואדודא	₹•												
236		(11)		A) N		KKV.	mig	r fe	atur	_							
237				B) L(						-							
238								TON	: /n	ote=	πpΒ	AG19!	5 ins	sert	: AS	heavy	
239			`-	-, ·				able			P						
240									5								
241		(xi)	SEC	OUEN	CE DI	ESCR	IPTIC	ON:	SEO :	ID NO	0:5:						
242		,															
243	ATG	GAC	TGG	ACC	TGG	AGG	GTC	TTC	TGC	TTG	CTG	GCT	GTA	GCA	CCA	GGT	48
244	Met	Asp	Trp	Thr	Trp	Arq	Val	Phe	Сув	Leu	Leu	Ala	Val	Ala	Pro	Gly	
245		-	_		_	_			_						-5	-	
246																	
247	GCC	CAC	TCC	CAG	GTC	CAA	CTG	CAG	GAG	AGC	GGT	CCA	GGT	CTT	GTG	AGA	96
248	Ala	His	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Arg	
249				1				5	_		_		10				
250																	
251																	
252	CCT	AGC	CAG	ACC	CTG	AGC	CTG	ACC	TGC	ACC	GCG	TCT	GGC	TTC	AAC	ATT	144
253	Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	
254		15					20					25					
255					•												
256	AAA	GAC	ACC	TAT	ATG	CAC	TGG	GTG	AGA	CAG	CCA	CCT	GGA	CGA	GGT	CTT	192
257	Lys	Asp	Thr	Tyr	Met	His	Trp	Val	Arg	Gln	Pro	Pro	Gly	Arg	Gly		
258	30					35					40					45	
259																	
260	GAG	TGG	ATT	GGA	AGG	ATT	GAT	CCT	GCG	AGT	GGC	GAT	ACT	AAA	TAT	GAC	240

### Raw Sequence Listing

04/08/93 07:45:48 S5136.raw

261 262 263	Glu	Trp	Ile	Gly	Arg 50	Ile	Asp	Pro	Ala	Ser 55	Gly	Asp	Thr	Lys	Tyr 60	Asp		
264	CCG	AAG	TTC	CAG	GTC	AGA	GTG	ACA	ATG	CTG	GTA	GAC	ACC	AGC	AGC	AAC	2	88
265				Gln														
266		•		65		•			70			-		75				
267																		
268	CAG	TTC	AGC	CTG	AGA	CTC	AGC	AGC	GTG	ACA	GCC	GCC	GAC	ACC	GCG	GTC	3	36
269	Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val		
270			80					85					90					
271																		
272	TAT	TAT	TGT	GCA	GAC	GGA	ATG	TGG	GTA	TCA	ACG	GGA	TAT	GCT	CTG	GAC	3	84
273	Tyr	Tyr	Сув	Ala	Asp	Gly	Met	Trp	Val	Ser	Thr	Gly	Tyr	Ala	Leu	Asp		
274		95					100					105						
275																		
276				CAA													4	29
277		Trp	Gly	Gln	Gly		Thr	Val	Thr	Val		Ser	Gly	Glu	Ser			
278	110					115					120							
279																		
280	(2)	INF	ORMA:	rion	FOR	SEQ	ID 1	10:6	:									
281																		
282			(i) 8	SEQUI														
283				•		NGTH:				acida	3							
284						PE: 8												
285				(D)	TOP	POLO	żΥ: .	Linea	ar									
286																		
207		1.	: : \ 1	YOT B	711T E2	TUDI	. n.		:									
287		(:	ii) 1	MOLE	CULE	TYPI	3: pi	rote:	in									
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288 289 290 291		(2	ki) £		ence	DESC	CRIPT	CION	: SE(	Leu			Val	Ala	Pro -5	Gly		
288 289 290 291 292	Met -19	(2	ki) £	SEQUI	ENCE Trp	DESC	CRIPT	CION	: SE(	_			Val	Ala		Gly		
288 289 290 291	-19	(s Asp	ki) {	SEQUI	Trp -15	DES(	CRIPT Val	rion Phe	: SE(	Leu -10	Leu	Ala			- 5			
288 289 290 291 292 293	-19	(s Asp	ki) {	SEQUI Thr	Trp -15	DES(	CRIPT Val	rion Phe	: SE(	Leu -10	Leu	Ala			- 5			
288 289 290 291 292 293 294	-19	(s Asp	ki) {	SEQUI Thr Gln	Trp -15	DES(	CRIPT Val	FION Phe Gln	: SE(	Leu -10	Leu	Ala	Gly		- 5			
288 289 290 291 292 293 294 295	-19 Ala	Asp His	ki) { Trp Ser	SEQUI Thr Gln	Trp -15	DESC Arg Gln	Val Leu	Phe Gln 5	: SE( Cys Glu	Leu -10 Ser	Leu Gly	Ala Pro	Gly 10	Leu	-5 Val	Arg		
288 289 290 291 292 293 294 295 296	-19 Ala	Asp His	ki) { Trp Ser	SEQUI Thr Gln 1	Trp -15	DESC Arg Gln	Val Leu	Phe Gln 5	: SE( Cys Glu	Leu -10 Ser	Leu Gly	Ala Pro	Gly 10	Leu	-5 Val	Arg		
288 289 290 291 292 293 294 295 296 297	-19 Ala	(2 Asp His	ki) { Trp Ser	SEQUI Thr Gln 1	Trp -15	DESC Arg Gln	Val Leu Leu	Phe Gln 5	: SE( Cys Glu	Leu -10 Ser	Leu Gly	Ala Pro Ser	Gly 10	Leu	-5 Val	Arg		
288 289 290 291 292 293 294 295 296 297 298	-19 Ala Pro	Asp His Ser	ci) s Trp Ser	SEQUI Thr Gln 1	Trp -15 Val	DESC Arg Gln Ser	Val Leu Leu 20	Phe Gln 5	Cys Glu Cys	Leu -10 Ser	Leu Gly Ala	Ala Pro Ser 25	Gly 10	Leu Phe	-5 Val Asn	Arg		
288 289 290 291 292 293 294 295 296 297 298 299 300 301	-19 Ala Pro	Asp His Ser	ci) s Trp Ser	Thr Gln 1	Trp -15 Val	DESC Arg Gln Ser	Val Leu Leu 20	Phe Gln 5	Cys Glu Cys	Leu -10 Ser	Leu Gly Ala	Ala Pro Ser 25	Gly 10	Leu Phe	-5 Val Asn	Arg		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302	-19 Ala Pro	Asp His Ser	ci) s Trp Ser	Thr Gln 1	Trp -15 Val	DESC Arg Gln Ser	Val Leu Leu 20	Phe Gln 5	Cys Glu Cys	Leu -10 Ser	Leu Gly Ala Pro	Ala Pro Ser 25	Gly 10	Leu Phe	-5 Val Asn	Arg Ile Leu		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303	-19 Ala Pro Lys 30	Asp His Ser 15	Trp Ser Gln	Thr Gln 1 Thr	Trp -15 Val Leu Met	DESC Arg Gln Ser His 35	Val Leu 20	Phe Gln 5 Thr	Cys Glu Cys Arg	Leu -10 Ser Thr	Leu Gly Ala Pro 40	Ala Pro Ser 25 Pro	Gly 10 Gly	Leu Phe Arg	-5 Val Asn Gly	Arg Ile Leu 45		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304	-19 Ala Pro Lys 30	Asp His Ser 15	Trp Ser Gln	Thr Gln 1	Trp -15 Val Leu Met	DESC Arg Gln Ser His 35	Val Leu 20	Phe Gln 5 Thr	Cys Glu Cys Arg	Leu -10 Ser Thr Gln	Leu Gly Ala Pro 40	Ala Pro Ser 25 Pro	Gly 10 Gly	Leu Phe Arg	-5 Val Asn Gly	Arg Ile Leu 45		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305	-19 Ala Pro Lys 30	Asp His Ser 15	Trp Ser Gln	Thr Gln 1 Thr	Trp -15 Val Leu Met	DESC Arg Gln Ser His 35	Val Leu 20	Phe Gln 5 Thr	Cys Glu Cys Arg	Leu -10 Ser Thr	Leu Gly Ala Pro 40	Ala Pro Ser 25 Pro	Gly 10 Gly	Leu Phe Arg	-5 Val Asn Gly	Arg Ile Leu 45		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306	-19 Ala Pro Lys 30 Glu	Asp His Ser 15 Asp	Trp Ser Gln Thr	Thr Gln 1 Thr Tyr	Trp -15 Val Leu Met	DESC Arg Gln Ser His 35	Val Leu 20 Trp	Phe Gln 5 Thr Val	Cys Glu Cys Arg	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40	Ala Pro Ser 25 Pro	Gly 10 Gly Thr	Leu Phe Arg	-5 Val Asn Gly Tyr 60	Arg Ile Leu 45		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307	-19 Ala Pro Lys 30 Glu	Asp His Ser 15 Asp	Trp Ser Gln Thr	Thr Gln 1 Thr Tyr Gly	Trp -15 Val Leu Met	DESC Arg Gln Ser His 35	Val Leu 20 Trp	Phe Gln 5 Thr Val	Cys Glu Cys Arg Ala	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40	Ala Pro Ser 25 Pro	Gly 10 Gly Thr	Leu Phe Arg Lys	-5 Val Asn Gly Tyr 60	Arg Ile Leu 45		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308	-19 Ala Pro Lys 30 Glu	Asp His Ser 15 Asp	Trp Ser Gln Thr	Thr Gln 1 Thr Tyr	Trp -15 Val Leu Met	DESC Arg Gln Ser His 35	Val Leu 20 Trp	Phe Gln 5 Thr Val	Cys Glu Cys Arg	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40	Ala Pro Ser 25 Pro	Gly 10 Gly Thr	Leu Phe Arg	-5 Val Asn Gly Tyr 60	Arg Ile Leu 45		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309	-19 Ala Pro Lys 30 Glu Pro	Asp His Ser 15 Asp Trp	Trp Ser Gln Thr	Thr Gln 1 Thr Tyr Gly Gln 65	Trp -15 Val Leu Met Arg 50 Val	DESC Arg Gln Ser His 35	Val Leu 20 Trp Asp	Phe Gln 5 Thr Val	Cys Glu Cys Arg Ala Met 70	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40 Gly Val	Ala Pro Ser 25 Pro Asp	Gly Gly Gly Thr	Leu Phe Arg Lys Ser 75	-5 Val Asn Gly Tyr 60 Ser	Arg Ile Leu 45 Asp		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310	-19 Ala Pro Lys 30 Glu Pro	Asp His Ser 15 Asp Trp	Trp Ser Gln Thr Ile Phe	Thr Gln 1 Thr Tyr Gly	Trp -15 Val Leu Met Arg 50 Val	DESC Arg Gln Ser His 35	Val Leu 20 Trp Asp	Phe Gln 5 Thr Val Pro Thr	Cys Glu Cys Arg Ala Met 70	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40 Gly Val	Ala Pro Ser 25 Pro Asp	Gly 10 Gly Thr	Leu Phe Arg Lys Ser 75	-5 Val Asn Gly Tyr 60 Ser	Arg Ile Leu 45 Asp		
288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309	-19 Ala Pro Lys 30 Glu Pro	Asp His Ser 15 Asp Trp	Trp Ser Gln Thr	Thr Gln 1 Thr Tyr Gly Gln 65	Trp -15 Val Leu Met Arg 50 Val	DESC Arg Gln Ser His 35	Val Leu 20 Trp Asp	Phe Gln 5 Thr Val	Cys Glu Cys Arg Ala Met 70	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40 Gly Val	Ala Pro Ser 25 Pro Asp	Gly Gly Gly Thr	Leu Phe Arg Lys Ser 75	-5 Val Asn Gly Tyr 60 Ser	Arg Ile Leu 45 Asp		

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313 314 315	Tyr	Tyr 95	Сув	Ala	Asp	Gly	Met 100	Trp	Val	Ser	Thr	Gly 105	Tyr	Ala	Leu	Asp	
316																	
317		Trp	Gly	Gln	Gly		Thr	Val	Thr	Val		Ser	Gly	Glu	Ser		
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320	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:7	:								
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338		(ix)	FE2	ATURI	₫:												
339		,,		A) NZ		KEY:	CDS										
340			-	-			13	386									
341			•	•													
342		(ix)	FE	ATURI	3:												
343			(2	A) NZ	AME/E	KEY:	misc	c fea	ature	9							
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348		(xi)	SE	QUENC	CE DE	SCR	PTIC	ON: S	SEQ :	ID NO	7:7:						
349																	
350	ATG	GGT	TGG	TCC	TGC	ATC	ATC	CTG	TTC	CTG	GTT	GCT	ACC	GCT	ACC	GGT	48
351		Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
352	-19				-15					-10					- 5		
353																	
354																	
355																	
356		CAC															96
357	val	His	ser		Ile	Val	Met		GIn	Ser	Pro	Ser		Leu	ser	Ala	
358				1				5					10				
359 360	300	are.	aam	a	202	ama	3.00	3 m ~	3.00	mar		~~~	3 Cm	~~	1 Cm	ama.	1 4 4
360 361		GTG															144
362	ser	Val 15	GTA	Asp	Arg	val	20	тте	inr	cys	гув	A1a 25	ber	GIU	ser	val	
363		13					20					45					
364	ልሮሞ	AAT	GAT	GTA	GCT	TGG	TAC	CAG	CAG	AAG	CCA	ርርጥ	DAG	сст	CCA	AAG	192
307	2207	WYI	GMI	GIM	GCI	196	inc	CAG	حمح	-AG	CCM	GGI	AAG	GCI	CCA	ANG	- 2 4

### Raw Sequence Listing

04/08/93 07:46:15 S5136.raw

366	THE	Asn	Asp	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys		
~ ~ -	30					35					40					45		
367																		
368	CTG	CTG	ATC	TAC	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGT	GTG	CCA	GAT	AGA		240
369	Leu	Leu	Ile	Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg		
370					50					55					60			
371																		
372	TTC	AGC	GGT	AGC	GGT	TAT	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC		288
373	Phe	Ser	Gly	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser		
374				65					70					75				
375																		
376	CTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	CAG	CAG	GAT	TAT	AGC		336
377	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Asp	Tyr	Ser		
378			80					85					90					
379																		
380	TCT	CCG	TAC	ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	CGT	AAG	TG	386
381	Ser	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Lys		
382		95	•			•	100	•		•		105		•	_	•		
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384	(2)	INFO	ORMA	TON	FOR	SEQ	TD 1	10 : 8 :										
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392 393 394 395		(3	ki) S	EQUI	емсе Сув	DESC	CRIPT	TION:	: SEÇ	Leu			Thr	Ala	Thr	Gly		
392 393 394 395 396	<b>Met</b> -19	(3	ki) S	EQUI	NCE	DESC	CRIPT	TION:	: SEÇ	-			Thr	Ala	Thr -5	Gly		
392 393 394 395 396 397	-19	(s Gly	ci) S Trp	SEQUI Ser	Cys -15	DES(	CRIP	rion: Leu	: SE(	Leu -10	Val	Ala			- 5			
392 393 394 395 396 397 398	-19	(s Gly	ci) S Trp	SEQUI Ser Ser	Cys -15	DES(	CRIP	TION: Leu Thr	: SE(	Leu -10	Val	Ala	Ser					
392 393 394 395 396 397 398 399	-19	(s Gly	ci) S Trp	SEQUI Ser	Cys -15	DES(	CRIP	rion: Leu	: SE(	Leu -10	Val	Ala			- 5			
392 393 394 395 396 397 398 399 400	-19 Val	() Gly His	ki) S Trp Ser	SEQUE Ser Ser 1	Cys -15	DESC Ile Val	CRIPT Ile Met	Leu Thr	: SE( Phe Gln	Leu -10 Ser	Val Pro	Ala Ser	Ser 10	Leu	-5 Ser	Ala		
392 393 394 395 396 397 398 399 400 401	-19 Val	Gly His	ki) S Trp Ser	SEQUE Ser Ser 1	Cys -15	DESC Ile Val	CRIPTION IN THE	Leu Thr	: SE( Phe Gln	Leu -10 Ser	Val Pro	Ala Ser Ala	Ser 10	Leu	- 5	Ala		
392 393 394 395 396 397 398 399 400 401 402	-19 Val	() Gly His	ki) S Trp Ser	SEQUE Ser Ser 1	Cys -15	DESC Ile Val	CRIPT Ile Met	Leu Thr	: SE( Phe Gln	Leu -10 Ser	Val Pro	Ala Ser	Ser 10	Leu	-5 Ser	Ala		
392 393 394 395 396 397 398 399 400 401 402 403	-19 Val Ser	Gly His Val	Trp Ser	Ser Ser Ser 1	Cys -15 Ile	DESC Ile Val	Ile Met Thr	Leu Thr 5	: SE( Phe Gln Thr	Leu -10 Ser	Val Pro Lys	Ala Ser Ala 25	Ser 10 Ser	Leu Gln	-5 Ser	Ala Val		
392 393 394 395 396 397 398 399 400 401 402 403 404	-19 Val Ser	Gly His Val	Trp Ser	Ser Ser Ser 1	Cys -15 Ile	DESC Ile Val Val	Ile Met Thr	Leu Thr 5	: SE( Phe Gln Thr	Leu -10 Ser	Val Pro Lys Pro	Ala Ser Ala 25	Ser 10 Ser	Leu Gln	-5 Ser	Ala Val Lys		
392 393 394 395 396 397 398 399 400 401 402 403 404 405	-19 Val Ser	Gly His Val	Trp Ser	Ser Ser Ser 1	Cys -15 Ile	DESC Ile Val	Ile Met Thr	Leu Thr 5	: SE( Phe Gln Thr	Leu -10 Ser	Val Pro Lys	Ala Ser Ala 25	Ser 10 Ser	Leu Gln	-5 Ser	Ala Val		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406	-19 Val Ser	Gly His Val	Trp Ser	Ser Ser Ser 1	Cys -15 Ile	DESC Ile Val Val	Ile Met Thr	Leu Thr 5	: SE( Phe Gln Thr	Leu -10 Ser	Val Pro Lys Pro	Ala Ser Ala 25	Ser 10 Ser	Leu Gln	-5 Ser	Ala Val Lys		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly	Ser Ser 1 Asp	Cys -15 Ile Arg	DESC Ile Val Val	Ile Met Thr 20	Thr 5	Phe Gln Thr	Leu -10 Ser Cys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala	-5 Ser Ser	Ala Val Lys 45		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly	Ser Ser 1 Asp	Cys -15 Ile Arg Ala	DESC Ile Val Val	Ile Met Thr 20	Thr 5	Phe Gln Thr	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala	-5 Ser Ser Pro	Ala Val Lys 45		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly	Ser Ser 1 Asp	Cys -15 Ile Arg	DESC Ile Val Val	Ile Met Thr 20	Thr 5	Phe Gln Thr	Leu -10 Ser Cys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala	-5 Ser Ser	Ala Val Lys 45		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly	Ser Ser 1 Asp	Cys -15 Ile Arg Ala	DESC Ile Val Val	Ile Met Thr 20	Thr 5	Phe Gln Thr	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala	-5 Ser Ser Pro	Ala Val Lys 45		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly Asp	Ser Ser 1 Asp Val	Cys -15 Ile Arg Ala Tyr 50	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr	Thr 5 Ile Gln	Phe Gln Thr Gln Arg	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala Pro	-5 Ser Ser Pro	Ala Val Lys 45		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly Asp	Ser Ser 1 Asp Val	Cys -15 Ile Arg Ala Tyr 50	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr	Thr 5 Ile Gln	Phe Gln Thr Gln Arg	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala Pro	-5 Ser Ser Pro	Ala Val Lys 45		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly Asp	Sequence Ser 1 Asp Val	Cys -15 Ile Arg Ala Tyr 50	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr	Thr 5 Ile Gln	E SE( Phe Gln Thr Gln Arg	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala Pro	-5 Ser Ser Pro	Ala Val Lys 45		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412	-19 Val Ser Thr 30 Leu	Gly His Val 15 Asn Leu Ser	Trp Ser Gly Asp	Ser Ser 1 Asp Val Tyr Ser 65	Cys -15 Ile Arg Ala Tyr 50	DESC Ile Val Val Trp 35	Thr 20 Tyr	Thr 5 Ile Gln Asn	Phe Gln Thr Gln Arg Asp 70	Leu -10 Ser Cys Lys Tyr 55 Phe	Val Pro Lys Pro 40 Thr	Ala Ser Ala 25 Gly Gly	Ser 10 Ser Lys Val	Leu Gln Ala Pro Ile 75	-5 Ser Ser Pro	Ala Val Lys 45 Arg		
392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	-19 Val Ser Thr 30 Leu	Gly His Val 15 Asn Leu Ser	Trp Ser Gly Asp	Ser Ser 1 Asp Val Tyr Ser 65	Cys -15 Ile Arg Ala Tyr 50	DESC Ile Val Val Trp 35	Thr 20 Tyr	Thr 5 Ile Gln Asn	Phe Gln Thr Gln Arg Asp 70	Leu -10 Ser Cys Lys Tyr 55 Phe	Val Pro Lys Pro 40 Thr	Ala Ser Ala 25 Gly Gly	Ser 10 Ser Lys Val	Leu Gln Ala Pro Ile 75	-5 Ser Ser Pro Asp 60	Ala Val Lys 45 Arg		

### Raw Sequence Listing

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#### Patent Application US/08/029,330

417 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys 418 95 100 105

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PAGE:

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/029,330

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